parental lines and heterozygous in the F_1 individual were identified. A sparse marker panel was developed as KASP for genotyping the F_2 lines for QTL mapping.

For nematode tolerance, one major QTL was detected on chrom 5 that explained 25% of the phenotypic variance. This QTL was further validated in an independent breeding panel of sugar beet breeding material. QTL mapping for cercospora resistance revealed a major QTL on chromosome 4 detected in three of the four locations tested and explaining up to 30% of the genetic variance.

DNA of F2 individuals at the extreme of the phenotypic distribution for the traits under consideration is currently combined into pools and sequenced with Illumina technology. Allele frequencies for variants will be determined for both pools. Deviations in allele frequencies between the pools should identify the genomic loci responsible for the quantitative traits. In order to pinpoint to the causal genes, the candidate regions will then be further analyzed with regard to e.g. functional gene annotation and the impact of variant positions in the diverse alleles.

W1018: Sugar Cane (ICSB)

Leveraging Multiple Sequencing Technologies to Generate a Haplotype Specific Assembly of Sugarcane R570

Adam Healey[1], John Lovell[2], Olivier Garsmeur[3], Jerry Jenkins[2], Jane Grimwood[2], Karen Aitken[4], Robert J. Henry[5], Angélique D'Hont[3], Jeremy Schmutz[2] and HudsonAlpha-Genome Sequencing Center, (1)HudsonAlpha Institute For Biotechnology, Huntsville, AL, (2)HudsonAlpha Institute for Biotechnology, Huntsville, AL, (3)CIRAD, UMR AGAP, Montpellier, France, (4)CSIRO Agriculture and Food, St Lucia, Australia, (5)University of Queensland/QAAFI, Brisbane, QLD, Australia

While sugarcane is one of the world's most important economic grasses for its sugar production and biofuel potential, tools and resources to understand its genetics are lacking. This is owed to the complexity of its genome which is highly polyploid, aneuploidy and heterozygous. Additionally, modern sugarcane cultivars are the result of interspecific hybridization and repeated backcrossing between domesticated *S. officinarium* and wild *S. spontaneum* parents. Cultivar R570 is best characterized sugarcane genome to date with the release of the BAC clone single tiling path, but this assembly represents a gene-rich and collapsed view of each of R570's homeologous chromosomes. To generate a haplotype specific assembly of R570, we devised a strategy that combines two *de novo* assemblies of R570 (Illumina; Pacbio), 96 selfed offspring (15X cov), single chromosome libraries and HiC to sequence and separate each homeologous chromosome. Using Illumina libraries, we generated a 5 Gb *de novo* genome assembly, using it to extract 55 Million unique 80bp genetic markers. Genotyping these markers in 96 selfed offspring isolated 1.9 million simplex (single dose) markers that were projected onto the 7.4 Gb PacBio assembly to generate a genetic map and anchor contigs onto separate linkage groups. Contigs that cannot be anchored by simplex markers will be ordered and oriented using HiC contact maps and single chromosome libraries. This strategy of combining multiple sequencing technologies will generate a more complete assembly for one of the most complex genomes to date in the Plant Kingdom.

W1019: Sugar Cane (ICSB)

Sequencing the Transcriptome of R570 to Explore the Complexity of the Sugarcane Genome

Adhini Sudhindra Kumar Pazhany[1], Virginie Perlo[2], Frikkie Botha[3], Agnelo Furtado[3], Angela O'Keeffe[4], Ardy Kharabian Masouleh[4], Robert Henry[5], Karen Aitken[6], Angelique d'Hont[7], Adam Healey[8], Jane Grimwood[9], Kerrie Barry[10] and Jeremy Schmutz[9], (1)Queensland Alliance for Agriculture and Food Innovation,The University of Queensland, St Lucia, QLD, Australia, (2)University of Queensland, Brisbane, Australia, (3)University of Queensland/QAAFI, Brisbane, QLD, Australia, (4)QAAFI (Queensland Alliance for Agriculture and Food Innovation), The University of Queensland, Brisbane, QLD, Australia, (5)Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD, Australia, (6)CSIRO Agriculture and Food, St Lucia, Australia,

(7)CIRAD (Centre de Coopération Internationale en Recherche Agronomique pour le Développement), Montpellier, France, (8)HudsonAlpha Institute For Biotechnology, Huntsville, AL, (9)HudsonAlpha Institute for Biotechnology, Huntsville, AL, (10)Department of Energy Joint Genome Institute, Walnut Creek, CA

Sugarcane is a crop of unequivocal importance which can meet requirements for food, feed fiber and fuel. This crop, with a large wealth of genetic resources and a rich breeding history, has only a very nascent genomic history with a monoploid genome sequence. Numerous efforts are underway to unravel the mysteries of this complex crop with advances in sequencing technologies. Efforts to capture the functional part of the genome using transcriptomic studies have long been a priority. R570, a French cultivar has been the most suitable material for many sugarcane genomics studies. In an attempt to utilize the revolutionary technology of long read sequencing, we have carried out isoform sequencing of this representative cultivar with a Pac Bio sequel I system. Recently we have compared sequel II data of the same cultivar from various vegetative and reproductive tissues. A greater sequencing depth may benefit the sugarcane fraternity with a more complete transcriptome and accurate gene annotation. The present study aimed at comparing sequel I and sequel II data for R570 to harness the information contained in the large transcriptome resources and to find novel sources of variation in the light of these recent advances. The results may support future transcriptomic studies in sugarcane to make informed decisions on depth of sequencing and help to unravel the complexities of this transcriptome.

W1020: Sugar Cane (ICSB)

Characterisation of Metabolic Regulation of Carbon Partitioning in the Sugarcane Culm through different Stages of Development using Transcriptome and Metabolome Data

Virginie Perlo[1], Frederik Botha[2], Agnelo Furtado[3] and Robert J. Henry[3], (1)University of Queensland, Brisbane, Australia, (2)QAAFI Queensland Alliance for Agriculture and Food Innovation - UQ University, St Lucia, QLD, Australia, (3)University of Queensland/QAAFI, Brisbane, QLD, Australia

Sugarcane has a high potential to be used to generate environmentally friendly by-products for use in chemical, pharmaceutical, medical, cosmetic and food industries. A crucial challenge for a long-term economic viability is to optimise the crop for production of a biomass composition that will ensure maximum economic benefit. Transcriptome data analysis provides a relevant explanation of phenotypic variances and gives a more accurate prediction of phenotypes than genomic information. This study of genetic variation in gene expression and correlations with metabolic data and phenotype relied on high-throughput methodology, measurement and analysis of 360 samples, 24 commercial sugarcane cultivars with different phenotypic characteristics at 5 different development stages with 3 replicates.

A multi-omic approach, with an integrated transcriptomics and metabolomics analysis may reveal details of biological mechanisms and pathways. A global view of transcriptional regulation and the identification of differentially expressed genes (DEGs) and metabolites may improve the feasibility of tailoring or engineering targeted biosynthetic pathways to improve the production of bio-products from sugarcane. We are using a profiling analysis workflow (pipeline) to generate empirical correlations between gene expression, metabolites, phenotypic traits and pathway analysis.

W1021: Sugar Cane (ICSB)

Investigation of the UDP-Glucose Metabolism in Sugarcane (*Saccharum* spp. hybrids)

Patrick J Mason[1], Frikkie Botha[1], Nam Hoang[1], Annelie Marquardt[1], Gabriella Papa[2], Jenny C. Mortimer[2], Agnelo Furtado[1], Blake Simmons[2] and Robert J. Henry[1], (1)University of Queensland/QAAFI, Brisbane, QLD, Australia, (2)Joint Bioenergy Instutute, San Francisco, CA

The synthesis and degradation of UDP-glucose is central to the amount of carbon (C) moving into the major pools within sugarcane, specifically sucrose, cellulose and hemicellulose. Knowledge regarding the differences in UDP-glucose metabolism and in turn C partitioning throughout the major organs within the sugarcane plant is still limited. The major organs of sugarcane roots, leaves and intermodal tissues